

**Notic to Comply**

Application No.

09/529,239

Examiner

David H Kruse

Applicant(s)

DOUTRIAUX ET AL.

Art Unit

1638

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other:

**Applicant Must Provide:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

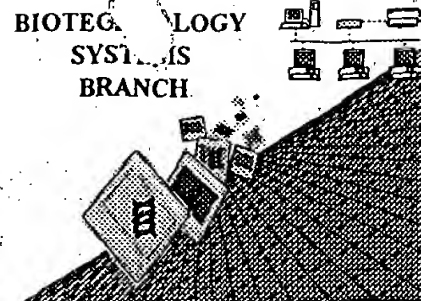
PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY**

## RAW SEQUENCE LISTING ERROR REPORT



#10/K.1  
7/5  
Raw  
Seq  
Listing  
(error)  
**RECEIVED**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/529,239

Source: 1638

Date Processed by STIC: 6-12-01

JUL 05 2001

TECH CENTER 1600/2900

### **THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

#### **PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

RECEIVED

JUL 05 2001

TECH CENTER 1600/2900

1638

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/529,239

DATE: 06/12/2001

TIME: 13:19:50

Input Set : A:\09529239SeqList.txt

Output Set: N:\CRF3\06122001\I529239.raw

Does Not Comply  
Corrected Diskette Needed

See pp. 1, 2, 5

2 <110> APPLICANT: Doutriaux, Marie-Pascale  
3 Betzner, Andreas  
4 Freyssinet, Georges  
5 Perez, Pascal  
7 <120> TITLE OF INVENTION: METHOD FOR OBTAINING PLANT VARIETIES  
10 <130> FILE REFERENCE: A33153-PCT-USA 072667.0128  
12 <140> CURRENT APPLICATION NUMBER: US 09/529,239  
C--> 13 <141> CURRENT FILING DATE: 2000-01-27  
15 <150> PRIOR APPLICATION NUMBER: PCT/EP98/06977  
16 <151> PRIOR FILING DATE: 1998-10-09  
18 <160> NUMBER OF SEQ ID NOS: 98

## ERRORED SEQUENCES

932 <210> SEQ ID NO: 26  
933 <211> LENGTH: 1385  
934 <212> TYPE: DNA  
935 <213> ORGANISM: Arabidopsis thaliana ecotype Columbia  
936 <223> OTHER INFORMATION: Clone 43  
938 <400> SEQUENCE: 26

→ Number of sequences differ.  
- 1385 listed  
- 2188 shown (see next page)

940	cccgggatgc agcgccagag atcgattttg tctttcttcc aaaaacccac ggcggcgact	60
941	acgaagggtt tggtttcgg cgatgctgct agcggcgggg gcggcagcgg aggaccacga	120
942	tttaatgtga aggaagggga tgctaaaggc gacgcttctg tacgttttgc tgtttcgaaa	180
943	tctgtcgatg aggttagagg aacggatact ccaccggaga aggttcgcgg tcgtgtcctg	240
944	ccgtctggat ttaagccggc tgaatccgcc ggtgatgctt cgtccctgtt ctccaatatt	300
945	atgcataagt ttgtaaaagt cgatgatcga gattgttctg gagagaggag ccgagaagat	360
946	gttggtccgc tgaatgattc atctctatgt atgaaggcta atgatgttat tcctcaattt	420
947	cgttccaata atggtaaaac tcaagaaaga aaccatgctt ttagtttcag tgggagagct	480
948	gaacttagat cagtagaaga tataaggagta gatggcgatg ttctgtgtcc agaaacacca	540
949	gggatgcgtc cagtgcttcc togttgaag cgagttcttg aggatgaaat gacttttaag	600
950	gaggataagg ttctgttatt ggactctaac aaaaggctga aaatgctcca ggatccgggt	660
951	tgtggagaga agaaagaagt aaacgaagga accaaatttg aatggcttga gtcttctcga	720
952	atcagggatg ccaatagaag acgtcctgat gatccccctt acgatagaaa gaccttacac	780
953	ataccacctg atgttttcaa gaaaatgtct gcatcacaaa agcaatattg gagtgttaag	840
954	agtgaatata tggacattgt gcttttcttt aaagtgggga aattttatga gctgtatgag	900
955	ctagatgcgg aattaggtca caaggagctt gactggaaga tgaccatgag tgggtgtggga	960
956	aaatgcagac aggttggtat ctctgaaagt gggatagatg aggcagtga aaagctatta	1020
957	gctcgtggat ataaagttgg acgaatcgag cagctagaaa catctgacca agcaaaagcc	1080
958	agaggtgcta ataactataat tccaaggaag ctagtccagg tattaactcc atcaacagca	1140
959	agcgagggaa acatcggggc tgatgccgtc catcttcttg ctataaaaga gatcaaaatg	1200
960	gagctacaaa agtggttcaac tgtgtatgga tttgcttttg ttgactgtgc tgccttgagg	1260
961	ttttgggttg ggtccatcag cgatgatgca tcatgtgctg ctcttgagc gttattgatg	1320
962	caggtttctc caaaggaagt gttatatgac agtaaagggc tatcaagaga agcacaaaag	1380
963	gctctaagga aatatacgtt gacagggtct acggcggtac agttggctcc agtaccacaa	1440
964	gtaatggggg atacagatgc tgcgtggagt agaaatataa tagaatctaa cggatacttt	1500
965	aaaggttctt ctgaatcatg gaactgtgct gttgatggtc taaatgaatg tgatgttgcc	1560

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/529,239

DATE: 06/12/2001

TIME: 13:19:50

Input Set : A:\09529239SeqList.txt

Output Set: N:\CRF3\06122001\I529239.raw

```

966 cttagtgtctc ttggagagct aattaatcat ctgtctaggc taaagctaga agatgtactt 1620
967 aagcatgggg atatttttcc ataccaagtt tacaggggtt gtctcagaat tgatggccag 1680
968 acgatggtaa atcttgagat atttaacaat agctgtgatg gtggtccttc agggaccttg 1740
969 tacaaatata ttgataactg tgtagtcca actggtaagc gactcttaag gaattggatc 1800
970 tgccatccac tcaaagatgt agaaagcatc aataaacggc ttgatgtagt tgaagaattc 1860
971 acggcaaact cagaaagtat gcaaatcact ggccagtatc tccacaaact tccagactta 1920
972 gaaagactgc tcggacgcat caagtctagc gttcgatcat cagcctctgt gttgctgct 1980
973 cttctgggga aaaaagtgtc gaaacaacga gttaaagcat ttgggcaaat tgtgaaagg 2040
974 ttcagaagtg gaattgatct gttgttggct ctacagaagg aatcaaatat gatgagttt 2100
975 ctttataaac tctgtaaact tcttatatta gtaggaaaaa gcgggctaga gttatttctt 2160

```

E--&gt; 976 tctcaattcg aagcagccat agatagcg

1013 &lt;210&gt; SEQ ID NO: 28

1014 &lt;211&gt; LENGTH: 34

1015 &lt;212&gt; TYPE: DNA

1016 &lt;213&gt; ORGANISM: Artificial sequence

1018 &lt;220&gt; FEATURE:

1019 &lt;223&gt; OTHER INFORMATION: MSH6 specific primer 2S8 for PCR using cDNA of Arabidopsis

thaliana

1020 ecotype Columbia

E--&gt; 1022 &lt;400&gt; SEQUENCE: 26

1024 atccccgggtt atttgggaac acagtaagag gatt 34

1341 &lt;210&gt; SEQ ID NO: 31

1342 &lt;211&gt; LENGTH: 1109

1343 &lt;212&gt; TYPE: PRT

1344 &lt;213&gt; ORGANISM: Arabidopsis thaliana ecotype Columbia

1345 &lt;223&gt; OTHER INFORMATION: Polypeptide MSH6

1347 &lt;400&gt; SEQUENCE: 31

1349 Met Gln Arg Gln Arg Ser Ile Leu Ser Phe Phe Gln Lys Pro Thr Ala

1350 1 5 10 15

1352 Ala Thr Thr Lys Gly Leu Val Ser Gly Asp Ala Ala Ser Gly Gly Gly

1353 20 25 30

1355 Gly Ser Gly Gly Pro Arg Phe Asn Val Arg Glu Gly Asp Ala Lys Gly

1356 35 40 45

1358 Asp Ala Ser Val Arg Phe Ala Val Ser Lys Ser Val Asp Glu Val Arg

1359 50 55 60

1361 Gly Thr Asp Thr Pro Pro Glu Lys Val Pro Arg Arg Val Leu Pro Ser

1362 65 70 75 80

1364 Gly Phe Lys Pro Ala Glu Ser Ala Gly Asp Ala Ser Ser Leu Phe Ser

1365 85 90 95

1367 Asn Ile Met His Lys Phe Val Lys Val Asp Asp Arg Asp Cys Ser Gly

1368 100 105 110

1370 Glu Arg Ser Arg Glu Asp Val Val Pro Leu Asn Asp Ser Ser Leu Cys

1371 115 120 125

1373 Met Lys Ala Asn Asp Val Ile Pro Gln Phe Arg Ser Asn Asn Gly Lys

1374 130 135 140

1376 Thr Gln Glu Arg Asn His Ala Phe Ser Phe Ser Gly Arg Ala Glu Leu

1377 145 150 155 160

1379 Arg Ser Val Glu Asp Ile Gly Val Asp Gly Asp Val Pro Gly Pro Glu

1380 165 170 175

1382 Thr Pro Gly Met Arg Pro Arg Ala Ser Arg Leu Lys Arg Val Leu Glu

2188

1385 listed.

Incorrect sequence i.d. number.

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/529,239

DATE: 06/12/2001

TIME: 13:19:50

Input Set : A:\09529239SeqList.txt

Output Set: N:\CRF3\06122001\I529239.raw

```

1383          180          185          190
1385 Asp Glu Met Thr Phe Lys Glu Asp Lys Val Pro Val Leu Asp Ser Asn
1386          195          200          205
1388 Lys Arg Leu Lys Met Leu Gln Asp Pro Val Cys Gly Glu Lys Lys Glu
1389          210          215          220
1391 Val Asn Glu Gly Thr Lys Phe Glu Trp Leu Glu Ser Ser Arg Ile Arg
1392 225          230          235          240
1394 Asp Ala Asn Arg Arg Arg Pro Asp Asp Pro Leu Tyr Asp Arg Lys Thr
1395          245          250          255
1397 Leu His Ile Pro Pro Asp Val Phe Lys Lys Met Ser Ala Ser Gln Lys
1398          260          265          270
1400 Gln Tyr Trp Ser Val Lys Ser Glu Tyr Met Asp Ile Val Leu Phe Phe
1401          275          280          285
1403 Lys Val Gly Lys Phe Tyr Glu Leu Tyr Glu Leu Asp Ala Glu Leu Gly
1404          290          295          300
1406 His Lys Glu Leu Asp Trp Lys Met Thr Met Ser Gly Val Gly Lys Cys
1407 305          310          315          320
1409 Arg Gln Val Gly Ile Ser Glu Ser Gly Ile Asp Glu Ala Val Gln Lys
1410          325          330          335
1412 Leu Leu Ala Arg Gly Tyr Lys Val Gly Arg Ile Glu Gln Leu Glu Thr
1413          340          345          350
1415 Ser Asp Gln Ala Lys Ala Arg Gly Ala Asn Thr Ile Ile Pro Arg Lys
1416          355          360          365
1418 Leu Val Gln Val Leu Thr Pro Ser Thr Ala Ser Glu Gly Asn Ile Gly
1419          370          375          380
1421 Pro Asp Ala Val His Leu Leu Ala Ile Lys Glu Ile Lys Met Glu Leu
1422 385          390          395          400
1424 Gln Lys Cys Ser Thr Val Tyr Gly Phe Ala Phe Val Asp Cys Ala Ala
1425          405          410          415
1427 Leu Arg Phe Trp Val Gly Ser Ile Ser Asp Asp Ala Ser Cys Ala Ala
1428          420          425          430
1430 Leu Gly Ala Leu Leu Met Gln Val Ser Pro Lys Glu Val Leu Tyr Asp
1431          435          440          445
1433 Ser Lys Gly Leu Ser Arg Glu Ala Gln Lys Ala Leu Arg Lys Tyr Thr
1434          450          455          460
1436 Leu Thr Gly Ser Thr Ala Val Gln Leu Ala Pro Val Pro Gln Val Met
1437 465          470          475          480
1439 Gly Asp Thr Asp Ala Ala Gly Val Arg Asn Ile Ile Glu Ser Asn Gly
1440          485          490          495
1442 Tyr Phe Lys Gly Ser Ser Glu Ser Trp Asn Cys Ala Val Asp Gly Leu
1443          500          505          510
1445 Asn Glu Cys Asp Val Ala Leu Ser Ala Leu Gly Glu Leu Ile Asn His
1446          515          520          525
1448 Leu Ser Arg Leu Lys Leu Glu Asp Val Leu Lys His Gly Asp Ile Phe
1449          530          535          540
1451 Pro Tyr Gln Val Tyr Arg Gly Cys Leu Arg Ile Asp Gly Gln Thr Met
1452 545          550          555          560
1454 Val Asn Leu Glu Ile Phe Asn Asn Ser Cys Asp Gly Gly Pro Ser Gly
1455          565          570          575

```

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Input Set : A:\09529239SeqList.txt

Output Set: N:\CRF3\06122001\I529239.raw

```

1457 Thr Leu Tyr Lys Tyr Leu Asp Asn Cys Val Ser Pro Thr Gly Lys Arg
1458          580          585          590
1460 Leu Leu Arg Asn Trp Ile Cys His Pro Leu Lys Asp Val Glu Ser Ile
1461          595          600          605
1463 Asn Lys Arg Leu Asp Val Val Glu Glu Phe Thr Ala Asn Ser Glu Ser
1464          610          615          620
1466 Met Gln Ile Thr Gly Gln Tyr Leu His Lys Leu Pro Asp Leu Glu Arg
1467 625          630          635          640
1469 Leu Leu Gly Arg Ile Lys Ser Ser Val Arg Ser Ser Ala Ser Val Leu
1470          645          650          655
1472 Pro Ala Leu Leu Gly Lys Lys Val Leu Lys Gln Arg Val Lys Ala Phe
1473          660          665          670
1475 Gly Gln Ile Val Lys Gly Phe Arg Ser Gly Ile Asp Leu Leu Leu Ala
1476          675          680          685
1478 Leu Gln Lys Glu Ser Asn Met Met Ser Leu Leu Tyr Lys Leu Cys Lys
1479          690          695          700
1481 Leu Pro Ile Leu Val Gly Lys Ser Gly Leu Glu Leu Phe Leu Ser Gln
1482 705          710          715          720
1484 Phe Glu Ala Ala Ile Asp Ser Asp Phe Pro Asn Tyr Gln Asn Gln Asp
1485          725          730          735
1487 Val Thr Asp Glu Asn Ala Glu Thr Leu Thr Ile Leu Ile Glu Leu Phe
1488          740          745          750
1490 Ile Glu Arg Ala Thr Gln Trp Ser Glu Val Ile His Thr Ile Ser Cys
1491          755          760          765
1493 Leu Asp Val Leu Arg Ser Phe Ala Ile Ala Ala Ser Leu Ser Ala Gly
1494          770          775          780
1496 Ser Met Ala Arg Pro Val Ile Phe Pro Glu Ser Glu Ala Thr Asp Gln
1497 785          790          795          800
1499 Asn Gln Lys Thr Lys Gly Pro Ile Leu Lys Ile Gln Gly Leu Trp His
1500          805          810          815
1502 Pro Phe Ala Val Ala Ala Asp Gly Gln Leu Pro Val Pro Asn Asp Ile
1503          820          825          830
1505 Leu Leu Gly Glu Ala Arg Arg Ser Ser Gly Ser Ile His Pro Arg Ser
1506          835          840          845
1508 Leu Leu Leu Thr Gly Pro Asn Met Gly Gly Lys Ser Thr Leu Leu Arg
1509          850          855          860
1511 Ala Thr Cys Leu Ala Val Ile Phe Ala Gln Leu Gly Cys Tyr Val Pro
1512 865          870          875          880
1514 Cys Glu Ser Cys Glu Ile Ser Leu Val Asp Thr Ile Phe Thr Arg Leu
1515          885          890          895
1517 Gly Ala Ser Asp Arg Ile Met Thr Gly Glu Ser Thr Phe Leu Val Glu
1518          900          905          910
1520 Cys Thr Glu Thr Ala Ser Val Leu Gln Asn Ala Thr Gln Asp Ser Leu
1521          915          920          925
1523 Val Ile Leu Asp Glu Leu Gly Arg Gly Thr Ser Thr Phe Asp Gly Tyr
1524          930          935          940
1526 Ala Ile Ala Tyr Ser Val Phe Arg His Leu Val Glu Lys Val Gln Cys
1527 945          950          955          960
1529 Arg Met Leu Phe Ala Thr His Tyr His Pro Leu Thr Lys Glu Phe Ala

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/529,239

DATE: 06/12/2001

TIME: 13:19:50

Input Set : A:\09529239SeqList.txt

Output Set: N:\CRF3\06122001\I529239.raw

```

1530          965          970          975
1532 Ser His Pro Arg Val Thr Ser Lys His Met Ala Cys Ala Phe Lys Ser
1533          980          985          990
1535 Arg Ser Asp Tyr Gln Pro Arg Gly Cys Asp Gln Asp Leu Val Phe Leu
1536          995          1000          1005
1538 Tyr Arg Leu Thr Glu Gly Ala Cys Pro Glu Ser Tyr Gly Leu Gln Val
1539      1010          1015          1020
1541 Ala Leu Met Ala Gly Ile Pro Asn Gln Val Val Glu Thr Ala Ser Gly
E--> 1542 1025          1030          1035          1040
1544 Ala Ala Gln Ala Met Lys Arg Ser Ile Gly Glu Asn Phe Lys Ser Ser
EOK> 1545          1045          1050          1055
1547 Glu Leu Arg Ser Glu Phe Ser Ser Leu His Glu Asp Trp Leu Lys Ser
EOK> 1548          1060          1065          1070
1550 Leu Val Gly Ile Ser Arg Val Ala His Asn Asn Ala Pro Ile Gly Glu
EOK> 1551          1075          1080          1085
1553 Asp Asp Tyr Asp Thr Leu Phe Cys Leu Trp His Glu Ile Lys Ser Ser
EOK> 1554      1090          1095          1100
1556 Tyr Cys Val Pro Lys
EOK> 1557 1105

```

Amino acid  
number cannot  
be under two  
amino acids.

Move one space  
to the right.

Remaining lines are shown as  
erred due to the one error  
at amino 1040.

↓  
Gly  
1040

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the  
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to  
<223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/529,239

DATE: 06/12/2001

TIME: 13:19:51

Input Set : A:\09529239SeqList.txt

Output Set: N:\CRF3\06122001\I529239.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:82 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2

L:976 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1385 Found:2188 SEQ:26

L:1022 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:28 differs:26

L:1542 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:31

M:332 Repeated in SeqNo=31